


```

DB 905 LPTCAVCLERMDS--VLAICNHSFHARCLQWAD-----NTCPVCR 945

RESULT 2
Y057_CAEEL STANDARD: PRT: 235 AA.
AC 009463;
DR 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 24.9 kDa protein Cl6Cl0.7 in chromosome III.
GN Cl6Cl0.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Lloyd C.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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-----
DR EMBL: 246787; CAA86745.1; -
DR Wormpep: C16C10.7; ZNF1498.
DR InterPro: IPR000306; Znf_FYVE.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Zinc-finger.
FT ZN_FING 26 67 RING-TYPE.
FT DOMAIN 121 124 POLY-GLY.
FT DOMAIN 169 172 POLY-ALA.
SQ SEQUENCE 235 AA; 24915 MW; 21A04AE951F6382A CRC64;

Query Match 33.1%; Score 97; DB 1; Length 235;
Best Local Similarity 40.0%; Pred. No. 3.7e-05;
Matches 18; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

OY 4 CTTCSDFDHSRDVAIHCGHPEHLQCLQWETAP-SRTCPQCR 47
DB 26 CNIC---LDAKDAVVSILCGHLFCMPCLSQMDLTRNNQVCPVCK 67

RESULT 3
MKR3_MOUSE STANDARD: PRT: 544 AA.
AC 060764;
DR 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 3 (Zinc-finger protein 127).
GN MKR3 OR ZFP127 OR ZNF127.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Pubmed=10196368;
RA Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A.,

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RA Driscoll D.J., Stewart C.L., Rinchik E.M., Nicholls R.D.;
RT "Imprinting of a RING zinc-finger encoding gene in the mouse
RT chromosome region homologous to the Prader-Willi syndrome genetic
RT region.";
RL Hum. Mol. Genet. 8:795-803(1999).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1 SIMILARITY: CONTAINS 3 C3H1-TYPE ZINC FINGERS.
-----
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-----
DR EMBL: U19106; AAA76863.1; -
DR MGD: MGI:99138; Zfp127.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00642; zf-CCCH; 3.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 3.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 98 116 C3H1-TYPE 1.
FT ZN_FING 280 298 C3H1-TYPE 2.
FT DOMAIN 302 329 MAKORIN-TYPE CVS-HIS.
FT ZN_FING 347 401 RING-TYPE.
FT ZN_FING 436 456 C3H1-TYPE 3.
SQ SEQUENCE 544 AA; 59444 MW; FF05B7D034C5EA9F CRC64;

Query Match 32.6%; Score 95.5; DB 1; Length 544;
Best Local Similarity 31.7%; Pred. No. 0.00013;
Matches 19; Conservative 9; Mismatches 21; Indels 11; Gaps 2;

OY 3 LCTICSDFFDHSRDA-----AIHCGHPEHLQCLQW-----FETAPSRTPQCRIOYG 51
DB 346 VCGICMEVVEYERADPTDRRGILFSCNHYCLKICIRMRMSATQFENRISKSCPCRVSSG 405

RESULT 4
GOL1_DROME STANDARD: PRT: 284 AA.
AC 006003;
DR 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Golliath protein (G1 proteio).
GN GOL OR G1 OR GL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TRISSUE-Embryo;
RA MEDLINE=93216124; Pubmed=8462875;
RA Bouchard M.L., Cole S.;
RT "The Drosophila melanogaster developmental gene g1 encodes a variant
RT zinc-finger motif protein.";
RL Gene 125:205-209(1993).
CC -1 FUNCTION: REGULATION OF GENE EXPRESSION DURING MESODERM FORMATION.
CC -1 PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
CC -1 SUBCELLULAR LOCATION: Nuclear.
CC -1 TISSUE SPECIFICITY: VISCERAL MESODERM AND PRIMORDIA OF SOMATIC
CC MUSCULATURE.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL; M97204; AAA28582.1; -
DR PIR; JCI495; JCI495.
DR FlyBase; FBgn0004919; gol.
DR InterPro; IPR001841; ZnF_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Developmental protein; Zinc-finger; Transcription regulation;
KW DNA-binding; Nuclear protein.
FT ZN_FING 126 167 RING-TYPE.
FT DOMAIN 208 259 GLN/PRO/SER-RICH.
SQ SEQUENCE 284 AA; 31973 MW; ECE2D5EDBALR2B CRC64;

Query Match 31.4%; Score 92; DB 1; Length 284;
Best Local Similarity 31.9%; Pred. No. 0.00019;
Matches 15; Conservative 8; Mismatches 22; Indels 2; Gaps 1;

QY 4 CTCTGDFDHSRDVAIHCGHTPHLOCLIQEFAPSTRCPQCR 50
Db 126 CALCIENVKPTDTRILPKHEPHKNCIDPWL--IEHRTCPMKLDV 170

RESULT 5
TTG3_HUMAN
ID TTG3_HUMAN STANDARD; PRT; 2025 AA.
AC P53804; P78476; P78477;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tetrairicopeptide repeat protein 3 (TPR repeat protein D).
GN TTC3 OR TPRD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96281123; PubMed=8724848;
RA Ohira M., Ootsuyama A., Suzuki E., Ichikawa H., Seki N.,
RA Nagase T., Nomura N., Ohki M.;
RT "Identification of a novel human gene containing the
RT tetrairicopeptide repeat domain from the Down syndrome region of
RT chromosome 21.";
RL DNA Res. 3:3-16(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal brain;
RX MEDLINE=97103476; PubMed=8947847;
RA Tsukahara F., Hattori M., Muraki T., Sakaki Y.;
RT "Identification and cloning of a novel cDNA belonging to
RT tetrairicopeptide repeat gene family from Down syndrome-critical
RT region 21q22.2.";
RL J. Biochem. 120:820-827(1996).
RN [3]
RP ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRPDI (SHOWN HERE), TRPDI
CC AND TRPDI1; SEEMS TO BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
CC -1- SIMILARITY: CONTAINS 4 TPR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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DR EMBL; D83077; BAA11769.1; -
DR EMBL; D84294; BAA12301.1; -
DR EMBL; D84295; BAA12302.1; -
DR EMBL; D84296; BAA12303.1; -
DR MIM; 602259; -
DR InterPro; IPR001440; TPR.
DR InterPro; IPR001841; ZnF_fing.
DR Pfam; PF00515; TPR; 4.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Repeat; TPR repeat; Zinc-finger; Alternative splicing.
FT REPEAT 231 264 TPR 1.
FT REPEAT 266 298 TPR 2.
FT REPEAT 536 572 TPR 3.
FT REPEAT 576 609 TPR 4.
FT ZN_FING 1957 1997 RING-TYPE.
FT DOMAIN 1957 1997 RING-TYPE.
FT DOMAIN 1020 1029 POLY-SER.
FT DOMAIN 1899 1902 POLY-LYS.
FT DOMAIN 1018 1029 ARG/LYS-RICH (BASIC).
FT DOMAIN 1172 1185 ARG/LYS-RICH (BASIC).
FT DOMAIN 1563 1579 ARG/LYS-RICH (BASIC).
FT VARSPLIC 1 233 MISSING (IN ISOFORM TRPDI1).
FT VARSPLIC 1 310 MISSING (IN ISOFORM TRPDI1).
SQ SEQUENCE 2025 AA; 229889 MW; 1B4BCAA3684B6253 CRC64;

Query Match 31.2%; Score 91.5; DB 1; Length 2025;
Best Local Similarity 37.0%; Pred. No. 0.0014;
Matches 17; Conservative 7; Mismatches 19; Indels 3; Gaps 2;

QY 2 SLCTGDFDHSRDVAIHCGHTPHLOCLIQEFAPSTRCPQCR 47
Db 1955 SSGEICHEVF-KSRNVAVLKCGHYHKGCPKQWLK--GGSACPACQ 1997

RESULT 6
MKR4_HUMAN
ID MKR4_HUMAN STANDARD; PRT; 485 AA.
AC Q13434;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 4 (Zinc-finger protein 127-Xp) (ZNF127-Xp).
GN MKR4 OR ZNF127L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hendrich B.D., Longstreet M., Gustashaw K., Nicholls R.D.,
RA Willard H.F.;
RT "An x-linked homologue of the autosomal imprinted gene ZNF127
RT escapes X chromosome inactivation.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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Page 5

ID	BLCL_HUMAN	STANDARD:	PRT:	474 AA.
AC	09UT18	09Y523; 09Y522;		
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Signal transduction protein CBL-C (SH3-binding protein CBL-C) (CBL-3).			
GN	CBLC OR CBL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (LONG FORM).			
RX	MEDLINE=20035821; PubMed=10571044;			
RA	Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., Yamamoto T.;			
RT	"Molecular cloning and characterization of a novel cbl-family gene,			
RL	cbl-c.";			
RP	Gene 239:145-154(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (LONG AND SHORT FORMS).			
RC	TISSUE=Pancratic adenocarcinoma;			
RX	MEDLINE=99289203; PubMed=10362357;			
RA	Keane M.M., Eitenberg S.A., Nau M.M., Banerjee P., Cuello M.,			
RT	Penninger J., Lipkowitz S.;			
RL	"cbl-3: a new mammalian cbl family protein.";			
CC	Oncogene 18:3365-3375(1999).			
CC	-1- FUNCTION: REGULATOR OF EGFR MEDIATED SIGNAL TRANSDUCTION.			
CC	-1- SUBUNIT: INTERACTS WITH A RESTRICTED RANGE OF SH3 DOMAIN PROTEINS.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (potential).			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A			
CC	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS.			
CC	-1- PTM: PHOSPHORYLATED ON TYROSINES BY EGFR.			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC	-----			
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CC	or send an email to license@slb-slb.ch).			
CC	-----			
DR	EMBL; AB028645; BAA86298.1; -			
DR	EMBL; AF117646; AAD34341.1; -			
DR	EMBL; AF117647; AAD34342.1; -			
DR	HSSP; P22681; 1B47.			
DR	InterPro; IPR003153; CBL_N.			
DR	InterPro; IPR000980; SH2.			
DR	InterPro; IPR001841; Znf_ring.			
DR	Pfam; PF02262; CBL_N.1.			
DR	Pfam; PF02761; CBL_N2.1.			
DR	Pfam; PF02762; CBL_N3.1.			
DR	Pfam; PF00097; ZF-C3HC4.1.			
DR	SMART; SM00184; RING.1.			
DR	SMART; SM00252; SH2.1.			
DR	PROSITE; PS00518; ZF_RING_1; 1.			
DR	PROSITE; PS00089; ZF_RING_2; 1.			
KW	Nuclear protein; Zinc finger; Phosphorylation; Alternative splicing			
FT	DOMAIN	89	92	NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

Query Match	30.0%	Score 88	DB 1	Length,474
Best Local Similarity	37.5%	Pred. No. 0.00095		
Matches 18	Conservative 9	Mismatches 17	Indels 4	Gaps 2

Db 350 LCKICA---ESNKKYKIEPCGHLCCCLAAW-OHSQOTCPFCRCI 393

RESULT 11

ID RN12_HUMAN STANDARD; PRT; 624 AA.

AC Q9NW2; Q9Y598;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE RING finger protein 12 (LIM domain interacting RING finger protein)

DE (RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen)

GN RNF12 OR RLM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20469411; PubMed=11013082;

RA Ostendorf H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J., Jenkins N.A., Fischer P., Bach I.

RT "Functional characterization of the gene encoding RLM, the corepressor of LIM homeodomain transcription factors.";

RL Genomics 69:120-130(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99438124; PubMed=10508479;

RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H., Jongsma V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T., Old L.J.

RT "Antigens recognized by autologous antibody in patients with renal cell carcinoma.";

RL Int. J. Cancer 83:456-464(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Niimura K., Watanabe T.

RT "NEDO human cDNA sequencing project.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE DEACETYLASE COREPRESSOR COMPLEX.

CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -1- CAUTION: REF.2 DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITION 134 AND 142.

CC

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CC

CC -----

CC EMBL: AJ271670; CAC14228.1; -

CC EMBL: AF155109; AAD42875.1; ALT_FRAME.

CC EMBL: AK001334; BAA91632.1; -

CC InterPro: IPR003837; Glu-TRNAGln.

CC InterPro: IPR002190; PHD.

CC InterPro: IPR001965; PHD.

CC InterPro: IPR001841; Znf_ring.

CC Pfam: PF02686; Glu-TRNAGln; 1.

CC Pfam: PF01454; MAGE; 1.

CC Pfam: PF00628; PHD; 1.

CC Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE: PSS0089; ZF_RING_2; 1.

KW Transcription regulation; Zinc-finger.

FT DOMAIN 422 506

FT ZN_FING 570 611

FT DOMAIN 453 481

FT DOMAIN 500 506

FT CONFLICT 126 126

FT CONFLICT 134 134

FT CONFLICT 144 145

FT CONFLICT 418 418

SQ SEQUENCE 624 AA; 68527 MW; DE3ADE09ACACBCF8 CRC64;

Query Match 30.0%; Score 88; DB 1; Length 624;

Best Local Similarity 27.7%; Pred. No. 0.0012;

Matches 13; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Oy 1 LSICCTGDFDHSRDVAIHCGHTPHLOCTIOWFETAPSRTPQCR 47

Db 567 LKTCVCTEYTEGKNLRLKPCSHETHVHCIDRWL--SENSTPCR 611

RESULT 12

ID Y055_CAEEL STANDARD; PRT; 409 AA.

AC Q09251;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 47.6 kDa protein Cl6C10.5 in chromosome III.

GN Cl6C10.5

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC SRRAN-BRISTOL N2;

RA Lloyd C.

RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC

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CC

CC -----

CC EMBL: Z46787; CAA86743.1; -

CC WormPep: Cl6C10.5; CE01496.

DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE: PS50089; ZF_RING_2; 1.

KW Hypothetical protein; Transmembrane; Zinc-finger.

FT ZN_FING 296 358

FT TRANSMEM 122 142

FT TRANSMEM 147 167

FT TRANSMEM 174 194

FT TRANSMEM 218 238

FT TRANSMEM 243 263

FT TRANSMEM 388 408

SQ SEQUENCE 409 AA; 47627 MW; 6AB33FC9D026C461 CRC64;

Query Match 29.9%; Score 87.5; DB 1; Length 409;

Best Local Similarity 26.9%; Pred. No. 0.00095;

Matches 18; Conservative 8; Mismatches 22; Indels 19; Gaps 2;

QY 3 LCRTCS---PFFDHSRDVAAI-----HCGHFFHLOCLIQWFETAPSRPC 43
 Db 295 VCAACGGRLDSEHVNADAVTTKMEDEDEKIKYKSCGHVFHEPFCIRGVVVGKIQTC 354
 44 PQCRIV 50
 355 PYCKERV 361

RESULT 13
 RAPS_TORCA STANDARD; PRT; 411 AA.
 ID RAPS_TORCA
 AC P09108;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 43 kDa receptor-associated protein of the synapse (RAPSYN)
 DE (Acetylcholine receptor-associated 43 kDa protein) (43 kDa postsynaptic protein).
 GN RAPSIN.
 OS Torpedo californica (Pacific electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalia; Hymnosqualia; Plistioraja; Batoidae;
 OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87317641; PubMed=3476945;
 RA Frail D.E., Mudd J., Shah V., Carr C., Cohen J.B., Merlie J.P.;
 RT "CDNAs for the postsynaptic 43-kDa protein of Torpedo electric organ encode two proteins with different carboxyl termini.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6302-6306(1987).
 RN [2]
 RP SEQUENCE OF 8-412.
 RX MEDLINE=88107644; PubMed=3427060;
 RA Carr C., McCourt D., Cohen J.B.;
 RT "The 43-kilodalton protein of Torpedo nicotinic postsynaptic membranes: purification and determination of primary structure.";
 RL Biochemistry 26:7090-7102(1987).
 RN [3]
 RP MYRISTOYLATION.
 RX MEDLINE=88331095; PubMed=3417776;
 RA Musil L.S., Carr C., Cohen J.B., Merlie J.P.;
 RT "Acetylcholine receptor-associated 43k protein contains covalently bound myristate.";
 RL J. Cell Biol. 107:1113-1121(1988).
 CC -1- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC MEMBRANES.
 CC -1- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO DISTINCT PROTEINS EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.
 CC -1- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC -1- SIMILARITY: BELONGS TO THE RAPSIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 DR EMBL: J02952; AAA49282.1; -;
 DR EMBL: J02953; AAA49283.1; -;
 DR PIR: A28009; A28009.

DR InterPro: IPR001237; Postsynaptic.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR001841; ZnF_Ring.
 DR Pfam: PF00515; TPR: 5.
 DR Pfam: PF00097; ZF-C3HC4; 1.
 DR PRINTS: PR00217; POSTSYNAPTIC.
 DR PRODOM: PD012428; Postsynaptic; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00028; TPR; 4.
 DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Synapse: Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 KM Myristate: zinc-finger; Alternative splicing.
 FT INIT MET 0
 FT ZN_FING 362 402 RING-TYPE.
 FT LIPID 1 1 MYRISTATE.
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT VARSPIC 404 404 PHOSPHORYLATION (POTENTIAL).
 FT VARSPIC 389 411 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 361 361 Y -> T (IN REF. 2).
 FT CONFLICT 393 393 N -> D (IN REF. 2).
 FT CONFLICT 410 410 Y -> T (IN REF. 2).
 SQ SEQUENCE 411 AA; 46321 MW; 4D26262679FC9BAD CRC64;

Query Match 29.98; Score 87.5; DB: 1; Length 411;
 Best Local Similarity 35.68; Pred. No. 0.00095;
 Matches 16; Conservative 9; Mismatches 15; Indels 5; Gaps 2;

QY 4 CTISDFE-HDSRDVAIHCGHFFHLOCLIQWFETAPSRPCPCR 47
 Db 362 CGLGESTIGDNGSLQALPCHLFLHACL-----QTNGRGCPNCK 402

RESULT 14
 BML_MOUSE STANDARD; PRT; 324 AA.
 ID BML_MOUSE
 AC P25916;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Polycarb complex protein BMI-1.
 GN BML1 OR BMI-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91249382; PubMed=1904009;
 RA Haupt Y., Alexander W.S., Bartl G., Klincken S.P., Adams J.M.;
 RT "Novel zinc finger gene implicated as myc collaborator by retrovirally accelerated lymphomagenesis in E mu-myc transgenic mice.";
 RL Cell 65:753-761(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91249381; PubMed=1904008;
 RA van Iohannizen M., Verbeek S., Scheijlen B., Wientjens E., Gulden H., Berns A.;
 RT "Identification of co-operating oncogenes in E mu-myc transgenic mice by provirus tagging.";
 RL Cell 65:737-752(1991).
 CC -1- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY.
 CC -1- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX (PCG).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: DETECTED IN MOST ORGANS WITH HIGH EXPRESSION LEVELS IN THYMUS, HEART, BRAIN AND TESTIS.
 CC -1- DISEASE: COOPERATES WITH THE MYC ONCOGENE TO PRODUCE B LYMPHOMAS.

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CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: M64067; AAA37299.1; -.
DR EMBL: M64068; AAA37301.1; ALT_SEQ.
DR EMBL: M64279; AAA37300.1; -.
DR PIR: A39523; A39523.
DR PIR: A39524; A39524.
DR MGD: MGI:88174; Bmi1.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Chromatin regulator; Nuclear protein; Transcription regulation;
KW Repressor; Zinc-finger; Proto-oncogene.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 249 324 PRO/SER-RICH.
SQ SEQUENCE 324 AA; 36707 MW; AD7DECD86B29DC55 CRC64;

Query Match 29.7%; Score 87; DB 1; Length 324;
Best Local Similarity 33.3%; Pred. No. 0.00088;
Matches 16; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

OY 3 LCTICSDPFHSDVAAIHGCHFHLOCLIQWTFAPSPRCPOCRIOV 50
Db 17 MCVLCGGYFIDATYI--TECLHSFCKTCIVRYLET--SKYCPIDVOY 60

RESULT 15
BMIT_HUMAN STANDARD; PRT; 326 AA.
AC P35226; Q96F37;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Polycarb complex protein Bmi-1.
CN BMIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MIML=94093545; PubMed=8268912;
RA Alkema M.J., Wiegand J., Raap A.K., Berns A., van Lohuizen M.;
RT "Characterization and chromosomal localization of the human proto-
RT oncogene Bmi-1.";
RL Hum. Mol. Genet. 2:1597-1603(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
CC STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
CC IN ITS EXPRESSIBILITY.
CC -1- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
CC (PCG).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: COOPERATES WITH THE MCG ONCOGENE TO PRODUCE B LYMPHOMAS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
```

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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: L13689; AAA19873.1; -.
DR EMBL: BC011652; AAH11652.1; -.
DR MIM: 164831; -.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Chromatin regulator; Nuclear protein; Transcription regulation;
KW Repressor; Zinc-finger; Proto-oncogene.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 251 326 PRO/SER-RICH.
FT CONFLICT 265 265 V->I (IN REF. 2).
SQ SEQUENCE 326 AA; 36935 MW; 1188BD396B2BA43 CRC64;

Query Match 29.7%; Score 87; DB 1; Length 326;
Best Local Similarity 33.3%; Pred. No. 0.00088;
Matches 16; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

OY 3 LCTICSDPFHSDVAAIHGCHFHLOCLIQWTFAPSPRCPOCRIOV 50
Db 17 MCVLCGGYFIDATYI--TECLHSFCKTCIVRYLET--SKYCPIDVOY 60

RESULT 16
Z147_MOUSE STANDARD; PRT; 634 AA.
AC 061510;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
GN ZNF147 OR ZFP147 OR EFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus, Ovary, and Placenta;
RX MEDLINE=96025835; PubMed=7592654;
RA Orino A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
RT "Molecular cloning, structure, and expression of mouse estrogen-
RT responsive finger protein Efp. Co-localization with estrogen receptor
RT mRNA in target organs.";
RL J. Biol. Chem. 270:24406-24413(1995).
CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
CC -----
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CC -----
DR EMBL: D63902; BAA09941.1; -.
DR MGD: MGI:102749; Zfp147.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
```


Query	3	LCITCSDF-----DHSRDVAALHCGHPTHDOCLIQ-----FETAPSRTCQCRI	48
Db	237	VCSTICMEVILTKASASERRFGILSCNNTYCLSCIRQWRCKAQGFNPITKSPCEERV	293
RESULT	18		
MR2_MOUSE		STANDARD:	PRT: 416 AA.
AC	OPERVL: Q9DOL9;		
DT	01-MAR-2002 (Rel. 41, Created)		
DT	01-MAR-2002 (Rel. 41, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Makorin 2.		
GN	MKNR2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21481893; PubMed=11597136;		
RA	Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.,		
RT	"Phylogenetic conservation of the makorin-2 gene, encoding a multiple		
RT	tzinc-finger protein, antisense to the raf1 proto-oncogene";		
RL	Genomics 77:119-126(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	STRAIN=C57BL/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; PubMed=1121851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Plesio G., Quackenbush J.,		
RA	Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner I., Mashio T.,		
RA	Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Guastacchi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kontenki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL: AF277171; MAG27596.1; -
DR EMBL: AK011295; BAB27523.1; -
DR MGI: 1914277; Mkr2.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf-Fing.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF00642; Zf-CCCH; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf-C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Repeat.
KM ZN_FING 8 C3H1-TYPE 1.
FT ZN_FING 37 C3H1-TYPE 2.
FT ZN_FING 171 189 C3H1-TYPE 3.
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 238 292 RING-TYPE.
FT ZN_FING 327 347 C3H1-TYPE 4.
FT CONFLICT 181 181 L -> F (IN REF. 2).
SQ SEQUENCE 416 AA; 46562 MW; 5F268EB9D9A6C9F CRC64;

Query Match 29.5%; Score 86.5; DB 1; Length 416;
Best Local Similarity 29.8%; Pred. No. 0.0013;
Matches 17; Conservative 10; Mismatches 19; Indels 11; Gaps 2;

OY 3 LCCTCSDFP-----DHSRDVAIHGCHTFHLOCLIOW-----RFTAPSRPCPCORI 48
Db 237 VCSICMEVILEKASASERRRIGILSNCSHTYCLSCIRWRCACAKOPENDPIINSCEPCRV 293

RESULT 19
YDRD_SCHPO STANDARD; PRT; 547 AA.
ID YDRD_SCHPO
AC 013747;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 61.8 kDa protein Cl6E8.13 in chromosome I.
GN SPAC16E8.13
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=912;
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YHLO10C AND C.ELEGANS REED8.9.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: Z98529; CAB11041.1; -
DR InterPro: IPR001841; Znf_Ring.
DR InterPro: IPR001607; Zf-UBP.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF02148; Zf-UBP; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00290; Znf-UBP; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE-NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Hypothetical protein; Zinc-finger.
FT ZN_FING 208 248 RING-TYPE.
FT DOMAIN 526 534 POLY-LYS.
SQ SEQUENCE 547 AA; 61825 MW; 2C3FDB4FD7CF70E1 CRC64;

Query Match 29.5%; Score 86.5; DB 1; Length 547;
Best Local Similarity 37.5%; Pred. No. 0.0017;
Matches 18; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

OY 1 LSLCTCSDFPDS-RVVAIHGCHTFHLOCLIOFWFTAPSRPCPCOR 47
Db 205 LPTCVCLERMDSITGLITIVCOHTRHCPCLQW-----GNSSCPVCR 248

RESULT 20
MEL18_MOUSE STANDARD; PRT; 342 AA.
ID MEL18_MOUSE
AC P23798;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE DNA-binding protein Mel-18.
GN ZNF144 OR ZFP144 OR ZFP-144 OR MEL18 OR MEL-18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91060627; PubMed=2246278;
RA Tagawa M., Sakamoto T., Shigemoto K., Matsubara H., Tamura Y.,
RA Ito T., Nakamura I., Okitsu A., Imai K., Taniguchi M.;
RT "Expression of novel DNA-binding protein with zinc finger structure
RT in various tumor cells".
RL J. Biol. Chem. 265:20021-20026(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=96091139; PubMed=8521824;
RA Kanno M., Hasegawa M., Ishida A., Isono K., Taniguchi M.;
RT "mel-18, a Polycomb group-related mammalian gene, encodes a
RT transcriptional negative regulator with tumor suppressive activity".
RL EMBO J. 14:5672-5678(1995).
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE
CC DNA SEQUENCE 5'GATGAGCT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY.
CC MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL
CC CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR CELLS AND
CC IN NEURAL TISSUES.
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED.
CC -1- DISEASE: PROBABLY RELATED TO TUMORGENESIS SINCE IT IS EXPRESSED
CC STRONGLY IN MOST TUMOR CELL LINES.


```

SO SEQUENCE 115 AA; 13241 MW; 745427AA3463DF71 CRC64;

Query Match 28.8%; Score 84.5; DB 1; Length 115;
Best Local Similarity 38.5%; Pred. No. 0.00068;
Matches 20; Conservative 6; Mismatches 17; Indels 9; Gaps 3;

OY 4 CTICSDFFDHSRD-----VAAIHGHFTFLHCLLIQWFTAPSRICPCRCIOY 50
      1 1 1 : : : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 44 CSIC--YNNYDEDEPLVVELPHCHHKEDLECLSYWL--SRSTTCPLCRDNV 91

RESULT 25
ID RAPS_CHICK STANDARD; PRT; 411 AA.
AC 042393;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 43 kDa receptor-associated protein of the synapse (RAPSYN)
DE (Acetylcholine receptor-associated 43 kDa protein) (43 kDa
DE postsynaptic protein).
GN RAPSN
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RC MEDLINE=97331014; PubMed=9185539;
RA Burns A.L., Benson D., Howard M.J., Margiotta J.F.;
RT "Chick ciliary ganglion neurons contain transcripts coding for
RT acetylcholine receptor-associated protein at synapses (rapyn).";
RL J. Neurosci. 17:5016-5026(1997).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
CC MEMBRANES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE FIBERS AND IN NEURONS.
CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
CC EMBL: AF000138; AAB63149.1; -.
CC InterPro: IPR001237; Postsynaptic.
CC InterPro: IPR001440; TPR.
CC InterPro: IPR001841; ZnF_Ring.
CC Pfam: PF00515; TPR; 6.
CC PRINTS: PR00217; POSTSYNAPTIC.
CC ProDom: PD012428; Postsynaptic; 1.
CC SMART: SM00184; RING_1.
CC SMART: SM00028; TPR; 5.
CC PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
CC Myristate; Zinc-finger.
CC INIT_MET 0 0 BY SIMILARITY.
CC ZN_FING 362 402 RING-TYPE.

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[illegible]

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DR EMBL: AF022081; AAC35248.1; -
 DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.
 FT ZN_FING 136 181 RING-TYPE.
 SQ SEQUENCE 194 AA; 21896 MW; 40C13970FC1DFF2 CRC64;

Query Match 28.7%; Score 84; DB 1; Length 194;
 Best Local Similarity 35.3%; Pred. No. 0.0013;
 Matches 18; Conservative 7; Mismatches 20; Indels 6; Gaps 2;

QY 4 CTC-----SFFDHSRDVAAIHCGHFTHLQCLIQWFTAPSRTCPCRCIOY 50
 Db 136 CPICMDGYSEIVONGRLIVSTECGHVFCSQLRDSLKNA--NTCPICRKRI 184

RESULT 29
 ICPO_HSVB7 STANDARD; PRT; 676 AA.

AC P29128;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trans-acting transcriptional protein ICPO (P135 protein) (IER
 DE 2.9/ER2.6).
 GN BICP0.
 OS Bovine herpesvirus type 1 (strain Jura).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxId=31518;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=92219360; PubMed=1313901;
 RA Wirth U V., Fraefel C., Vogt B., Vlack C., Paces V., Schwyzler M.;
 RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
 RT are 3' coterminal and encode a putative zinc finger transactivator
 RT protein.";
 RL J. Virol. 66:2763-2772(1992).

CC -1- PTM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
 CC ACTIVATION DOMAIN. POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
 CC CASEIN KINASE II.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.

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DR EMBL: M84465; AAA46061.1; -
 DR EMBL: AJ004801; CAA06138.1; -
 DR PIR: B38209; EDBE23.
 DR HSSP: P28990; ICNC.

DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
 KW

KW DNA-binding; Early protein; Repressor; Phosphorylation.
 FT ZN_FING 13 52 RING-TYPE.
 FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
 SQ SEQUENCE 676 AA; 67879 MW; 11B06BA4E5C4B71 CRC64;

Query Match 28.7%; Score 84; DB 1; Length 676;
 Best Local Similarity 38.0%; Pred. No. 0.0042;
 Matches 19; Conservative 5; Mismatches 22; Indels 4; Gaps 2;

QY 1 LSLCTICSDFFDHSRDVAAIHCGHFTHLQCLIQWFTAPSRTCPCRCIOY 50
 Db 10 LGSCCICLDIAITGA--ARALPCLHAFCLACIRRWLEGRP--TCPLCKAPV 55

RESULT 30
 ICPO_HSVBK STANDARD; PRT; 676 AA.

AC P29836;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trans-acting transcriptional protein ICPO (P135 protein) (IER
 DE 2.9/ER2.6).
 GN BICP0.
 OS Bovine herpesvirus type 1 (strain K22).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxId=31519;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=92219360; PubMed=1313901;
 RA Wirth U V., Fraefel C., Vogt B., Vlack C., Paces V., Schwyzler M.;
 RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
 RT are 3' coterminal and encode a putative zinc finger transactivator
 RT protein.";
 RL J. Virol. 66:2763-2772(1992).

CC -1- PTM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
 CC ACTIVATION DOMAIN. POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
 CC CASEIN KINASE II.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.

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DR EMBL: M84464; AAA46061.1; -
 DR PIR: A38209; EDBE22.
 DR HSSP: P28990; ICNC.

DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
 KW DNA-binding; Early protein; Repressor; Phosphorylation.
 FT ZN_FING 13 52 RING-TYPE.
 FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
 SQ SEQUENCE 676 AA; 67701 MW; 9BB0683CBFCA65D CRC64;

Query Match 28.7%; Score 84; DB 1; Length 676;
 Best Local Similarity 38.0%; Pred. No. 0.0042;
 Matches 19; Conservative 5; Mismatches 22; Indels 4; Gaps 2;

QY 1 LSLCTICSDFFDHSRDVAAIHCGHFTHLQCLIQWFTAPSRTCPCRCIOY 50
 Db 10 LGSCCICLDIAITGA--ARALPCLHAFCLACIRRWLEGRP--TCPLCKAPV 55

RESULT 31
 CBLB_HUMAN STANDARD; PRT; 982 AA.
 ID CBLB_HUMAN
 AC 013191; 013192; 013193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Signal transduction protein CBL-B (SH3-binding protein CBL-B).
 GN CBLB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95303504; PubMed=7784085;
 RA Keane M.M., Rivero-Lezcano O.M., Mitchell J.A., Robbins K.C.,
 RA Lipkowitz S.;
 RT "Cloning and characterization of cbl-b: a SH3 binding protein with
 RT homology to the c-cbl proto-oncogene";
 RL Oncogene 10:2367-2377(1995).
 CC -1- SUBUNIT: INTERACTS WITH SH3 DOMAIN PROTEINS FYN, FGR AND PLCG1.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN HERE), BY
 CC TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, KIDNEY, SPLEEN, AND TESTIS,
 CC AS WELL AS FETAL BRAIN AND LIVER AND HEMATOPOIETIC CELL LINES, BUT
 CC NOT IN ADULT BRAIN, LIVER, PANCREAS, SALIVARY GLAND, OR SKELETAL
 CC MUSCLE.
 CC -1- PTM: PHOSPHORYLATED ON TYROSINES.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.
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 CC -----
 DR EMBL: U26710; AAB09291.1; -
 DR EMBL: U26711; AAB09292.1; -
 DR EMBL: U26712; AAB09293.1; -
 DR HSSP: P22681; 1B47.
 DR MIM: 604491; -
 DR InterPro: IPR003153; Cbl_N.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR000449; UBA.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF02262; Cbl_N; 1.
 DR Pfam: PF02761; Cbl_N2; 1.
 DR Pfam: PF02762; Cbl_N3; 1.
 DR Pfam: PF00627; UBA; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Nuclear protein; zinc-finger; Phosphorylation; Alternative splicing.
 FT DOMAIN 116 119 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT ZN_FING 373 412 RING-TYPE.
 FT DOMAIN 477 701 PRO-RICH.
 FT DOMAIN 931 970 UBA.
 FT VARSPPLIC 812 982 MISSING (IN TRUNCATED ISOFORM 1).
 FT VARSPPLIC 767 770 DVED -> TVRI (IN TRUNCATED ISOFORM 2).
 FT VARSPPLIC 771 982 MISSING (IN TRUNCATED ISOFORM 2).
 SQ SEQUENCE 982 AA; 109479 MW; 038D4565DAFB98CB CRC64;

Query Match 28.7%; Score 84; DB 1; Length 982;
 Best Local Similarity 35.4%; Pred. No. 0.0059;
 Matches 17; Conservative 8; Mismatches 19; Indels 4; Gaps 2;
 Oy 3 LCYTCSDFPDSRDVAIHCGHFFHLOCIQWFEAPASRTCPQCRIOV 50
 Db 372 LCRICA---ENDRDVXIEPCGHMCTSLRWQOE-SDGQCCPCRCREI 415
 RESULT 32
 RAPS_HUMAN STANDARD; PRT; 411 AA.
 ID RAPS_HUMAN
 AC 013702;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 43 kDa receptor-associated protein of the synapse (RAPSIN)
 DE (Acetylcholine receptor-associated 43 kDa protein) (43 kDa
 DE postsynaptic protein).
 GN RAPSIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=97001170; PubMed=8812503;
 RA Buckel A., Beeson D., James M., Vincent A.;
 RT "Cloning of cDNA encoding human rapsyn and mapping of the RAPSIN gene
 RT locus to chromosome 11p11.2-p11.1";
 RL Genomics 35:613-616(1996).
 CC -1- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
 CC MEMBRANES.
 CC -1- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
 CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC -1- SIMILARITY: BELONGS TO THE RAPSIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL: Z33905; CAA83954.1; -
 DR MIM: 601592; -
 DR InterPro: IPR001237; Postsynaptic.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00515; TPR; 5.
 DR PRINTS: PR00217; POSTSYNAPTIC.
 DR PRODOM: PD012428; Postsynaptic; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00028; TPR; 5.
 DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ZN_FING 362 402 RING-TYPE.
 FT LIPID 1 195 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).

SQ SEQUENCE 411 AA; 46199 MW; 6A9FBA4B95E8C6C CRC64;
 Query Match 28.5%; Score 83.5; DB 1; Length 411;
 Best Local Similarity 33.3%; Pred. No. 0.003;
 Matches 15; Conservative 10; Mismatches 15; Indels 5; Gaps 2;
 OY 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCR 47
 Db 362 CALCGESIGENKSRRLQALPCSHIFHLKCL-----ONNGTRSCPNCR 402
 RESULT 33
 A33_PLEMA STANDARD; PRT; 624 AA.
 AC 002084;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc-binding protein A33.
 OS Pleurodeles waltliti (Iberian ribbed newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
 OC Pleurodeles.
 NC NCBI_Taxid=8319;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA MEDLINE=93154311; PubMed=7679068;
 RA Bellini M., Lacroix J.-C., Gall J.G.;
 RT "A putative zinc-binding protein on lampbrush chromosome loops.";
 RL EMO J. 12:107-114(1993).
 CC -1- FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED
 IN THE GERMINAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS
 AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-MRNA
 DURING OOGENESIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS
 AND IN THE NUCLEOPASM OF THE GERMINAL VESICLE (GV). IT IS
 TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBRYONIC
 NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT
 ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L04190; AAA49614.1; -
 DR InterPro: IPR003649; Bbox.C.
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003878; SPRY_domain.
 DR InterPro: IPR000315; znf_bbox.
 DR InterPro: IPR001841; znf_fing.
 DR Pfam; PF00622; SPRY.1.
 DR Pfam; PF00643; zfp-B_box.1.
 DR Pfam; PF00097; zfp-C3HC4.1.
 DR PRINTS; PR01406; BBOXZNFINGER.
 DR SMART; SM00502; BBC.1.
 DR SMART; SM00336; BBOX.1.
 DR SMART; SM00184; RING.1.
 DR SMART; SM00449; SPRY.1.
 DR PROSITE; PS50119; ZF_BBOX.1.
 DR PROSITE; PS00518; ZF_RING.1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Zinc-finger; Nuclear protein; Developmental protein; Coiled coil;

KW RNA-binding. 19 26
 FT DOMAIN 134 149
 FT ZN_FING 162 202
 FT ZN_FING 238 269
 FT DOMAIN 337 386
 FT DOMAIN 449 619
 SQ SEQUENCE 624 AA; 71056 MW; 60DBD1F3F071EFDD CRC64;
 Query Match 28.5%; Score 83.5; DB 1; Length 624;
 Best Local Similarity 29.5%; Pred. No. 0.004;
 Matches 13; Conservative 12; Mismatches 16; Indels 3; Gaps 1;
 OY 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCR 47
 Db 162 CPLCRSLF---KEPVILECGHNFCKHCIDKRSWESASAFSCPECK 202
 RESULT 34
 RNFE_HUMAN STANDARD; PRT; 685 AA.
 ID RNFE_HUMAN
 AC Q9Y252; Q9YF41;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RA MEDLINE=99265977; PubMed=10331950;
 RA Macdonald D.H.C., Lahiri D., Sampath A., Chase A., Sohal J.,
 RA Cross N.C.P.;
 RT "Cloning and characterization of RNFE6, a novel RING finger gene
 mapping to 13q12.";
 RL Genomics 58:94-97(1999).
 RN [2]
 RP SEQUENCE OF 320-685 FROM N.A.
 RC TISSUE=Testis;
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- TISSUE SPECIFICITY: WEAKLY EXPRESSED IN PERIPHERAL BLOOD, SPLEEN,
 PROSTATE, TESTIS AND OVARY.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 DR EMBL; AJ010347; CAB40414.1; -
 DR EMBL; AJ010346; CAB40413.1; -
 DR EMBL; AL133621; CAB63747.1; -
 DR HSSP; P28990; ICHC.
 DR MTR; 604242; -
 DR InterPro: IPR001841; znf_fing.
 DR Pfam; PF00097; zfp-C3HC4.1.
 DR SMART; SM00184; RING.1.
 DR PROSITE; PS00518; ZF_RING.1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Zinc-finger.
 FT DOMAIN 292 424
 FT DOMAIN 598 601
 FT ZN_FING 632 673
 SQ SEQUENCE 685 AA; 78091 MW; 344584773F2E5ERC CRC64;

DR SMART; SM00028; TPR; 3.
 DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 MYristate; Zinc-finger.
 FT INIT_MET 0
 FT ZN_RING 362 402 RING-TYPE.
 FT LIPID 1 1 MYRISTATE.
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
 FT CONFLICT 343 344 DV -> EL (IN REF. 2).
 SQ SEQUENCE 411 AA; 46233 MW; 1085A5C709FD156 CRC64;

Query Match 28.2%; Score 82.5; DB 1; Length 411;
 Best Local Similarity 33.3%; Pred. No. 0.004;
 Matches 15; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 4 CTICSDFF-DHSRDVAIHCGHTFHLOCLIQWETAPSRTPCPCR 47
 ID 362 CGLGGESIGERNRLQALPCSHIFHLRCL-----QNNCTRSCPNCR 402

RESULT 37
 YUES_CAEEL STANDARD; PRT; 564 AA.
 AC P90859; P90852;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 64.7 kDa protein F26E4.11 in chromosome 1.
 GN F26E4.11.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
 OC Rhabditidae; Peloderae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-BRISTOL NZ;
 RA Lightning J., Baynes C.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 CC
 DR EMBL: Z81070; CAB03009.1; -;
 DR EMBL: Z81075; CAB03009.1; JOINED.
 DR EMBL: Z81075; CAB03049.1; -;
 DR EMBL: Z81070; CAB03049.1; JOINED.
 DR WormPep: F26E4.11; CE096955.
 DR InterPro: IPR003892; CUE.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF02845; CUE; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00546; CUE; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Zinc-finger.
 FT ZN_RING 335 373 RING-TYPE.
 SQ SEQUENCE 564 AA; 64709 MW; 7C790C238207E49B CRC64;

Query Match 28.2%; Score 82.5; DB 1; Length 564;
 Best Local Similarity 34.0%; Pred. No. 0.0054;
 Matches 16; Conservative 6; Mismatches 20; Indels 5; Gaps 2;

QY 4 CTICSDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCPCR 50
 ID 335 CVVCEWELGSR---RLPCSHQHDWCLMWMW--ADSSCPICRCIT 376

RESULT 38
 MKRL_MACEU STANDARD; PRT; 478 AA.
 ID MKRL_MACEU
 AC Q9T91;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Makorin 1.
 GN MKRN1.
 OS Macropus eugenii (Tammam wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20304755; PubMed=10843807;
 RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
 RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
 RT "The ancient source of a distinct gene family encoding proteins
 RT featuring RING and C(3)H zinc-finger motifs with abundant expression
 RT in developing brain and nervous system."
 RL Genomics 66:76-86(2000).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL: AF192786; AAP17489.1; -;
 DR InterPro: IPR001395; Aldo_ket_red.
 DR InterPro: IPR000571; Zf-CCCH.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00642; zf-CCCH; 4.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00356; Znf_C3H1; 4.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Zinc-finger; Repeat.
 FT ZN_RING 57 75 C3H1-TYPE 1.
 FT ZN_RING 86 104 C3H1-TYPE 2.
 FT ZN_RING 210 228 C3H1-TYPE 3.
 FT DOMAIN 232 259 MAKORIN-TYPE CVS-HIS.
 FT ZN_RING 277 331 RING-TYPE.
 FT ZN_RING 366 386 C3H1-TYPE 4.
 SQ SEQUENCE 478 AA; 52905 MW; CB2D9B147433853E CRC64;

Query Match 27.8%; Score 81.5; DB 1; Length 478;
 Best Local Similarity 29.8%; Pred. No. 0.0061;
 Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;

QY 3 LCTICSDFF-----DHSRDVAIHCGHTFHLOCLIQWETAPSRTPCPCR 48
 ID 276 VCGICMEVVEKANSERRFGILSCNHTYCLKICRWRSAKOFESKIIKSCPECRI 332

RESULT 39
 MKRL_MOUSE STANDARD; PRT; 481 AA.
 ID MKRL_MOUSE
 AC Q9QXP6;
 DT 01-MAR-2002 (Rel. 41, Created)

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DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 1.
GN MKRNL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20304755; PubMed=10843807;
RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RT "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF192785; AAF17488.1; -
DR MGD: MGI:1859353; Mkrnl.
DR InterPro: IPR000571; Zf-CCCH.
DR DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00642; zf-CCCH; 4.
DR SMART: SM00356; ZNF_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Repeat.
KW ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
FT ZN_FING 481 AA; 53008 MW; B6BDE5E785CEAE CRC64;
SQ SEQUENCE

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Query Match 27.8%; Score 81.5; DB 1; Length 481;
Best Local Similarity 29.8%; Pred. No. 0.0062;
Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;
OY 3 LCITCSDFF-----DHSRDVAIHCGHTFLDCLLIOW-----FETAPSTPCPCRI 48
DB 280 VCGICMEVYEKANPSERRRFGILSNCHNYCLCKIRKWSAKOFESKIIKSCPCRI 336

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RESULT 40
MKRL_HUMAN STANDARD; PRT; 482 AA.
AC Q9UHC7; Q9UEZ7; Q9H0G0;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 1.
GN MKRNL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20304755; PubMed=10843807;

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RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RT "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansojge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Oltmannseder B., Obermaier B., Tampe J., Heubner D.,
RA Wombolt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF192784; AAF17487.1; -
DR EMBL: AF192793; AAF18979.1; -
DR EMBL: AF192789; AAF18979.1; JOINED.
DR EMBL: AF192790; AAF18979.1; JOINED.
DR EMBL: AF192791; AAF18979.1; JOINED.
DR EMBL: AF192792; AAF18979.1; JOINED.
DR EMBL: AL136812; CAB6746.1; -
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00642; zf-CCCH; 4.
DR SMART: SM00184; Zf-CCCH; 4.
DR SMART: SM00356; ZNF_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Repeat; Polymorphism.
KW ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
FT ZN_FING 481 AA; 53363 MW; C993DECD131691C CRC64;
SQ SEQUENCE

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Query Match 27.8%; Score 81.5; DB 1; Length 482;
Best Local Similarity 29.8%; Pred. No. 0.0062;
Matches 17; Conservative 11; Mismatches 18; Indels 11; Gaps 2;
OY 3 LCITCSDFF-----DHSRDVAIHCGHTFLDCLLIOW-----FETAPSTPCPCRI 48
DB 280 VCGICMEVYEKANPSERRRFGILSNCHNYCLCKIRKWSAKOFESKIIKSCPCRI 336

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